

## AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

1. (currently amended) A method of identifying bacteria, comprising:
  - a) providing:
    - i) amplified genomic sequences from a plurality of bacterial species, wherein said amplified genomic sequences are arrayed on a solid support so as to create a plurality of arrayed elements,
    - ii) labeled target DNA from test bacteria of interest, and
    - iii) labeled reference DNA from at least four strains of reference bacteria, wherein said reference bacteria are members of the group consisting of said plurality of bacterial species;
  - b) co-hybridizing said target and reference DNA to said arrayed elements in a single step to produce a hybridization pattern, wherein each hybridized target DNA in said hybridization pattern has a target signal, and each hybridized reference DNA in said hybridization pattern has a reference signal; and
  - c) calculating the target signal to reference signal hybridization ratio at each array element to determine the identity of said test bacteria.
2. (original) The method of Claim 1, wherein said test bacteria are from a sample obtained from a subject.
3. (original) The method of Claim 1, wherein said test bacteria are pathogenic organisms.
4. (original) The method of Claim 1, wherein said test bacteria are environmental isolates.
5. (original) The method of Claim 1, wherein said solid support is a microchip.

6. (original) The method of Claim 1, wherein said calculating comprises statistical analysis.
7. (previously presented) The method of Claim 1, wherein said target signal and said reference signal comprise fluorescence.
8. (original) The method of Claim 1, further comprising the step of producing hybridization profiles of said test and reference bacteria.
9. (currently amended) A method of identifying bacteria, comprising:
  - a) providing:
    - i) amplified genomic sequences from a plurality of bacterial species, wherein said amplified genomic sequences are arrayed on at least one microchip, so as to create a plurality of arrayed elements,
    - ii) labeled target DNA from test bacteria of interest, and
    - iii) labeled reference DNA from at least four strains of reference bacteria, wherein said reference bacteria are members of the group consisting of said plurality of bacterial species;
  - b) co-hybridizing said target and reference DNA to said arrayed elements in a single step to produce a hybridization pattern, wherein each hybridized target DNA in said hybridization pattern has a target signal, and each hybridized reference DNA in said hybridization pattern has a reference signal; and
  - c) calculating the target signal to reference signal hybridization ratio at each array element to determine the identity of said test bacteria.
10. (original) The method of Claim 9, wherein said test bacteria are from a sample obtained from a subject.

11. (original) The method of Claim 10, wherein said test bacteria are pathogenic organisms.
12. (original) The method of Claim 9, wherein said test bacteria are environmental isolates.
13. (original) The method of Claim 9, further comprising the step of producing hybridization profiles of said test and reference bacteria.
14. (original) The method of Claim 9, wherein said calculating comprises statistical analysis.
15. (previously presented) The method of Claim 9, wherein said target signal and said reference signal comprise fluorescence.
- 16 - 21 (canceled)